



- 1 -

SEQUENCE LISTING

<110> Evans, Glen A.

<120> Non-Immunoglobulin Binding Polypeptides

<130> 66663-026

<140> US 10/611,655

<141> 2003-06-30

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 162

<212> PRT

<213> Homo sapiens

<400> 1

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		20						25				30			
Ser	Leu	Arg	Leu	Asp	Cys	Arg	His	Glu	Asn	Thr	Ser	Ser	Ser	Pro	Ile
		35				40						45			
Gln	Tyr	Glu	Glu	Ser	Leu	Thr	Arg	Glu	Thr	Lys	Lys	His	Val	Leu	Phe
	50					55						60			
Gly	Thr	Val	Gly	Val	Pro	Glu	His	Thr	Tyr	Arg	Ser	Arg	Thr	Asn	Phe
65					70					75				80	
Thr	Ser	Lys	Tyr	His	Met	Lys	Val	Leu	Tyr	Leu	Ser	Ala	Phe	Thr	Ser
				85				90						95	
Lys	Asp	Glu	Gly	Thr	Tyr	Thr	Cys	Ala	Leu	His	His	Ser	Gly	His	Ser
		100						105					110		
Pro	Pro	Ile	Leu	Ser	Ser	Gln	Asn	Val	Thr	Val	Leu	Arg	Asp	Lys	Leu
		115					120					125			
Val	Lys	Cys	Glu	Gly	Ile	Ser	Leu	Leu	Ala	Gln	Asn	Thr	Ser	Trp	Leu
	130					135					140				
Leu	Leu	Leu	Leu	Leu	Ser	Leu	Ser	Leu	Leu	Gln	Ala	Thr	Asp	Phe	Met
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Ser	Leu														

<210> 2

<211> 124

<212> PRT

<213> Homo sapiens

<400> 2

Gln Leu Gln Gln Ser Gly Glu Ala Leu Val Lys Pro Gly Ala Ser Val

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Arg Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Pro Asn Tyr Trp Met
      20             25             30
His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Thr
      35             40             45
Ile Asp Pro Ala Asp Ser Tyr Thr Ser Tyr Asn Gln Asn Phe Lys Asp
      50             55             60
Lys Ala Thr Leu Thr Val Lys Pro Ser Ser Thr Ala Tyr Met Gln Leu
      65             70             75             80
Ser Ser Leu Thr Phe Gly Asp Ser Ala Val Tyr Phe Cys Ala Arg Glu
      85             90             95
Ser Tyr Tyr Tyr Arg Tyr Tyr Phe Asp Tyr Trp Gly His Gly Thr Thr
      100            105            110
Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu
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<210> 3
 <211> 37
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus peptide

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<400> 3
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Asn Phe Lys Asp Ala Thr Thr Ser Ile Ser Ser Glu Gly Ile Trp Leu
      20             25             30
Ser Leu Ser Thr Leu
      35

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<210> 4
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ThyOx non-immunoglobulin binding polypeptide

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<400> 4
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Asp Gln Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser Ser Ser
      20             25             30
Asn Tyr Trp Met His Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val
      35             40             45
Leu Phe Gly Thr Ile Asp Pro Ala Asp Ser Tyr Thr Ser Tyr Asn Gln
      50             55             60
Asn Phe Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His His Ser Gly
      65             70             75             80
His Ser Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys
      85             90             95

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Leu Val Lys Cys Glu Gly Val Tyr Tyr Arg Tyr Tyr Phe Asp Tyr
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<210> 5

<211> 1050

<212> DNA

<213> Artificial Sequence

<220>

<223> carrier encoding erythropoietin

<221> CDS

<222> (21)...(1022)

<400> 5

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Leu Leu Leu Ser Leu Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly
15 20 25

gcc ccc ccc cgg ctg atc tgc gac agc cgg gtg ctg gag cgg cac ctg 149
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg His Leu
30 35 40

ctg gag gcc aag gag gcc gag agc atc acc acc ggc tgc gtg gag gac 197
Leu Glu Ala Lys Glu Ala Glu Ser Ile Thr Thr Gly Cys Val Glu Asp
45 50 55

tgc agc ctg aac gag aac atc acc gtg ccc gac agc aag gtg aac ttc 245
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Ser Lys Val Asn Phe
60 65 70 75

tac gcc tgg aag cgg atg gag gtg ggc cag cag gcc gtg gag gtg tgg 293
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
80 85 90

cag ggc ctg gcc ctg ctg agc gag gcc gtg ctg cgg ggc cag gcc ctg 341
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
95 100 105

ctg gtg atc agc agc cag ccc tgg gag ccc ctg cag ctg cac gtg gac 389
Leu Val Ile Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
110 115 120

aag gcc gtg agc ggc ctg cgg agc ctg acc acc ctg ctg cgg gcc ctg 437
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
125 130 135

ggc gcc cag aag gag gcc atc agc ccc ccc gac gcc gcc agc gcc gcc 485
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala

140	145	150	155	
ccc ctg cgg acc atc acc gcc gac acc ttc cgg aag ctg ttc cgg gtg				533
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val				
	160	165	170	
tac ccc aac ttc ctg cgg ggc aag ctg aag ttc tac acc ggc gag gcc				581
Tyr Pro Asn Phe Leu Arg Gly Lys Leu Lys Phe Tyr Thr Gly Glu Ala				
	175	180	185	
tgc cgg ggc ggc ggc ggc ggc agc ggc ggc ggc ggc gag ttc ggc ggc				629
Cys Arg Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Glu Phe Gly Gly				
	190	195	200	
ggc ggc agc cag aag gtg acc agc ctg acc gcc tgc ctg gtg gac cag				677
Gly Gly Ser Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln				
	205	210	215	
agc ctg cgg ctg gac tgc cgg cac gag aac acc agc agc agc ccc atc				725
Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser Ser Ser Pro Ile				
	220	225	230	235
cag tac gag ttc agc ctg acc cgg gag acc aag aag cac gtg ctg ttc				773
Gln Tyr Glu Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe				
	240	245	250	
ggc acc gtg ggc gtg ccc gag cac acc tac cgg agc cgg acc aac ttc				821
Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe				
	255	260	265	
acc agc aag tac cac atg aag gtg ctg tac ctg agc gcc ttc acc agc				869
Thr Ser Lys Tyr His Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser				
	270	275	280	
aag gac gag ggc acc tac acc tgc gcc ctg cac cac agc ggc cac agc				917
Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His His Ser Gly His Ser				
	285	290	295	
ccc ccc atc agc agc cag aac gtg acc gtg ctg cgg gac aag ctg gtg				965
Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys Leu Val				
	300	305	310	315
aag tgc gag ggc atc agc ctg ctg gcc cag aac acc agc cac cac cac				1013
Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn Thr Ser His His His				
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His His His				

<210> 6

<211> 334

<212> PRT

<213> Artificial Sequence

<220>

<223> chimeric ThyOx carrier polypeptide containing
erythropoietin

<400> 6

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			20					25						30	
Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	His	Leu	Leu	Glu	Ala	Lys	Glu
		35					40					45			
Ala	Glu	Ser	Ile	Thr	Thr	Gly	Cys	Val	Glu	Asp	Cys	Ser	Leu	Asn	Glu
	50					55					60				
Asn	Ile	Thr	Val	Pro	Asp	Ser	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg
65					70					75					80
Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu
				85					90					95	
Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Ile	Ser	Ser
			100					105					110		
Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly
		115					120					125			
Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu
	130					135					140				
Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile
145					150					155					160
Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Pro	Asn	Phe	Leu
				165					170					175	
Arg	Gly	Lys	Leu	Lys	Phe	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Gly	Gly	Gly
		180						185					190		
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Glu	Phe	Gly	Gly	Gly	Gly	Ser	Gln	Lys
		195					200					205			
Val	Thr	Ser	Leu	Thr	Ala	Cys	Leu	Val	Asp	Gln	Ser	Leu	Arg	Leu	Asp
	210					215					220				
Cys	Arg	His	Glu	Asn	Thr	Ser	Ser	Ser	Pro	Ile	Gln	Tyr	Glu	Phe	Ser
225					230					235					240
Leu	Thr	Arg	Glu	Thr	Lys	Lys	His	Val	Leu	Phe	Gly	Thr	Val	Gly	Val
				245					250					255	
Pro	Glu	His	Thr	Tyr	Arg	Ser	Arg	Thr	Asn	Phe	Thr	Ser	Lys	Tyr	His
			260					265					270		
Met	Lys	Val	Leu	Tyr	Leu	Ser	Ala	Phe	Thr	Ser	Lys	Asp	Glu	Gly	Thr
		275					280					285			
Tyr	Thr	Cys	Ala	Leu	His	His	Ser	Gly	His	Ser	Pro	Pro	Ile	Ser	Ser
	290					295					300				
Gln	Asn	Val	Thr	Val	Leu	Arg	Asp	Lys	Leu	Val	Lys	Cys	Glu	Gly	Ile
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<210> 7

<211> 1050

<212> DNA

<213> Artificial Sequence

<220>

<223> SuperEpo

<221> CDS

<222> (21)...(1022)

<400> 7

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Leu Leu Leu Ser Leu Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly	
15 20 25	
gcc ccc ccc cgg ctg atc tgc gac agc cgg gtg ctg gag cgg cac ctg	149
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg His Leu	
30 35 40	
ctg gag gcc aag gag gcc gag agc atc acc acc ggc tgc gtg gag gac	197
Leu Glu Ala Lys Glu Ala Glu Ser Ile Thr Thr Gly Cys Val Glu Asp	
45 50 55	
tgc agc ctg aac gag aac atc acc gtg ccc gac agc aag gtg aac ttc	245
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Ser Lys Val Asn Phe	
60 65 70 75	
tac gcc tgg aag cgg atg gag gtg ggc cag cag gcc gtg gag gtg tgg	293
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp	
80 85 90	
cag ggc ctg gcc ctg ctg agc gag gcc gtg ctg cgg ggc cag gcc ctg	341
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu	
95 100 105	
ctg gtg atc agc agc cag ccc tgg gag ccc ctg cag ctg cac gtg gac	389
Leu Val Ile Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp	
110 115 120	
aag gcc gtg agc ggc ctg cgg agc ctg acc acc ctg ctg cgg gcc ctg	437
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu	
125 130 135	
ggc gcc cag aag gag gcc atc agc ccc ccc gac gcc gcc agc gcc gcc	485
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala	
140 145 150 155	
ccc ctg cgg acc atc acc gcc gac acc ttc cgg aag ctg ttc cgg gtg	533
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val	
160 165 170	

tac ccc aac ttc ctg cgg ggc aag ctg aag ttc tac acc ggc gag gcc	581
Tyr Pro Asn Phe Leu Arg Gly Lys Leu Lys Phe Tyr Thr Gly Glu Ala	
175 180 185	
tgc cgg ggc ggc ggc ggc ggc agc ggc ggc ggc ggc gag ttc ggc ggc	629
Cys Arg Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Glu Phe Gly Gly	
190 195 200	
ggc ggc agc cag aag gtg acc agc ctg acc gcc tgc ctg gtg gac cag	677
Gly Gly Ser Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln	
205 210 215	
agc ctg cgg ctg gac tgc cgg cac gag aac acc agc agc agc ccc atc	725
Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser Ser Ser Pro Ile	
220 225 230 235	
cag tac gag ttc agc ctg acc cgg gag acc aag aag cac gtg ctg ttc	773
Gln Tyr Glu Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe	
240 245 250	
ggc acc gtg ggc gtg ccc gag cac acc tac cgg agc cgg acc aac ttc	821
Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe	
255 260 265	
acc agc aag tac cac atg aag gtg ctg tac ctg agc gcc ttc acc agc	869
Thr Ser Lys Tyr His Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser	
270 275 280	
aag gac gag ggc acc tac acc tgc gcc ctg cac cac agc ggc cac agc	917
Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His His Ser Gly His Ser	
285 290 295	
ccc ccc atc agc agc cag aac gtg acc gtg ctg cgg gac aag ctg gtg	965
Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys Leu Val	
300 305 310 315	
aag tgc gag ggc atc agc ctg ctg gcc cag aac acc agc cac cac cac	1013
Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn Thr Ser His His His	
320 325 330	
cac cac cac tgatgataag atcggatcct aggcttcc	1050
His His His	

<210> 8

<211> 334

<212> PRT

<213> Artificial Sequence

<220>

<223> SuperEpo

<400> 8

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          20           25           30
Ile Cys Asp Ser Arg Val Leu Glu Arg His Leu Leu Glu Ala Lys Glu
          35           40           45
Ala Glu Ser Ile Thr Thr Gly Cys Val Glu Asp Cys Ser Leu Asn Glu
          50           55           60
Asn Ile Thr Val Pro Asp Ser Lys Val Asn Phe Tyr Ala Trp Lys Arg
65           70           75           80
Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
          85           90           95
Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Ile Ser Ser
          100          105          110
Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
          115          120          125
Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
          130          135          140
Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145          150          155          160
Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Pro Asn Phe Leu
          165          170          175
Arg Gly Lys Leu Lys Phe Tyr Thr Gly Glu Ala Cys Arg Gly Gly Gly
          180          185          190
Gly Gly Ser Gly Gly Gly Gly Glu Phe Gly Gly Gly Gly Ser Gln Lys
          195          200          205
Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln Ser Leu Arg Leu Asp
          210          215          220
Cys Arg His Glu Asn Thr Ser Ser Ser Pro Ile Gln Tyr Glu Phe Ser
225          230          235          240
Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe Gly Thr Val Gly Val
          245          250          255
Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe Thr Ser Lys Tyr His
          260          265          270
Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser Lys Asp Glu Gly Thr
          275          280          285
Tyr Thr Cys Ala Leu His His Ser Gly His Ser Pro Pro Ile Ser Ser
          290          295          300
Gln Asn Val Thr Val Leu Arg Asp Lys Leu Val Lys Cys Glu Gly Ile
305          310          315          320
Ser Leu Leu Ala Gln Asn Thr Ser His His His His His His
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<210> 9

<211> 600

<212> DNA

<213> Artificial Sequence

<220>

<223> carrier encoding glucagon-like peptide 1

<221> CDS

<222> (29)...(556)

<400> 9

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tct gac gtt tct tct tac ctg gaa ggt cag gcg gcg aaa gag ttc atc	100
Ser Asp Val Ser Ser Tyr Leu Glu Gly Gln Ala Ala Lys Glu Phe Ile	
10 15 20	
gcg tgg ctg gtt aaa ggt cgt ggt ggt ggt ggt ggt tct ggt ggt ggt	148
Ala Trp Leu Val Lys Gly Arg Gly Gly Gly Gly Gly Ser Gly Gly Gly	
25 30 35 40	
ggt gag ttc ggt ggt ggt ggt tct cag aaa gtt acc tct ctg acc gcg	196
Gly Glu Phe Gly Gly Gly Gly Ser Gln Lys Val Thr Ser Leu Thr Ala	
45 50 55	
tgc ctg gtt gac cag tct ctg cgt ctg gac tgc cgt cac gaa aac acc	244
Cys Leu Val Asp Gln Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr	
60 65 70	
tct tct tct ccg atc cag tac gag ttc tct ctg acc cgt gaa acc aaa	292
Ser Ser Ser Pro Ile Gln Tyr Glu Phe Ser Leu Thr Arg Glu Thr Lys	
75 80 85	
aaa cac gtt ctg ttc ggt acc gtt ggt gtt ccg gaa cac acc tac cgt	340
Lys His Val Leu Phe Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg	
90 95 100	
tct cgt acc aac ttc acc tct aaa tac cac atg aaa gtt ctg tac ctg	388
Ser Arg Thr Asn Phe Thr Ser Lys Tyr His Met Lys Val Leu Tyr Leu	
105 110 115 120	
tct gcg ttc acc tct aaa gac gaa ggt acc tac acc tgc gcg ctg cac	436
Ser Ala Phe Thr Ser Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His	
125 130 135	
cac tct ggt cac tct ccg ccg atc tct tct cag aac gtt acc gtt ctg	484
His Ser Gly His Ser Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu	
140 145 150	
cgt gac aaa ctg gtt aaa tgc gaa ggt atc tct ctg ctg gcg cag aac	532
Arg Asp Lys Leu Val Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn	
155 160 165	
acc tct cac cac cac cac cac cac tgataatgag atcttgaggc cggatccgct	586
Thr Ser His His His His His His	
170 175	
taagatcccg gcaa	600

<210> 10
 <211> 176
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> chimeric ThyOx carrier polypeptide containing
 glucagon-like peptide 1

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 20 25 30
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 35 40 45
 Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln Ser Leu Arg
 50 55 60
 Leu Asp Cys Arg His Glu Asn Thr Ser Ser Ser Pro Ile Gln Tyr Glu
 65 70 75 80
 Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe Gly Thr Val
 85 90 95
 Gly Val Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe Thr Ser Lys
 100 105 110
 Tyr His Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser Lys Asp Glu
 115 120 125
 Gly Thr Tyr Thr Cys Ala Leu His His Ser Gly His Ser Pro Pro Ile
 130 135 140
 Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys Leu Val Lys Cys Glu
 145 150 155 160
 Gly Ile Ser Leu Leu Ala Gln Asn Thr Ser His His His His His His
 165 170 175

<210> 11
 <211> 4000
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> vector pEgea M3

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 aagtgtatca tatgccaagt acgcccccta ttgacgtcaa tgacggtaaa tggcccgctt 240
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 tgggcggtag gcgtgtacgg tgggaggtct atataagcag agctctctgg ctaactagaa 540
 tcgaaattaa tacgactcac tatagggaga cccaagctgg ctacggttta aacttaagct 600

tgggtaccgag	ctcggatcca	ctctaggggg	tatccccacg	cgccctgtag	cggcgcatta	660
agcgcggcgg	gtgtgggtgt	tacgcgcagc	gtgaccgcta	cacttgccag	cgccctagcg	720
cccgcctcctt	tcgcttttctt	cccttccttt	ctcgccacgt	tcgccggctt	tccccgtcaa	780
gctctaaatc	gggggctccc	tttaggggttc	cgatttagtg	ctttacggca	cctcgacccc	840
aaaaaacttg	attaggggtga	tggttcacgt	agtgggcat	cgccctgata	gacggttttt	900
cgccctttga	cgttggagtc	cacgttcttt	aatagtggac	tcttgttcca	aactggaaca	960
acactcaacc	ctatctcggt	ctattctttt	gatttataag	ggattttgcc	gatttcggcc	1020
tattggttaa	aaaatgagct	gatttaacaa	aaatttaacg	cgaattaatt	ctgtggaatg	1080
tgtgtcagtt	agggtgtgga	aagtcctccag	gctccccagc	aggcagaagt	atgcaaagca	1140
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gtatgcaaag	catgcattctc	aattagtcag	caaccatagt	cccgccccta	actccgcccc	1260
tccccccct	aactccgccc	agttccgccc	attctccgcc	ccatggctga	ctaatttttt	1320
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Document: Sequence Listing pages 1-13

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